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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:40:42 ; Search time 20.26 Seconds

(without alignments)  
475.872 Million cell updates/sec

Title: US-09-502-984B-37  
Perfect score: 1284  
Sequence: 1 KFESKALLIARGPELLCF.....RKNERLEPEVERLKLQYNGR 249

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1060	82.6	508	1	EPOR_HUMAN
2	877.5	68.3	507	1	EPOR_RAT
3	869.5	67.7	507	1	EPOR_MOUSE
4	171	13.3	625	1	TPOR_MOUSE
5	146	11.4	635	1	TPOR_HUMAN
6	118	9.2	581	1	PRUR_BOVIN
7	116	9.0	831	1	PRUR_BOVIN
8	114.5	8.9	522	1	ILIR_MELGA
9	112.5	8.8	634	1	ILIR_BOVIN
10	110.5	8.6	634	1	GHR_BOVIN
11	110	8.6	831	1	PRUR_CHICK
12	108	8.4	281	1	PRUR_CHICK
13	108	8.4	581	1	PRUR_CEREL
14	107	8.3	608	1	GHR_CHICK
15	104.5	8.1	611	1	GHR_COLLI
16	104	8.1	616	1	PRUR_RABIT
17	103.5	8.1	650	1	GHR_MOUSE
18	103.5	8.1	830	1	PRUR_COLLI
19	103	8.0	638	1	GHR_MOUSE
20	99.5	7.7	638	1	GHR_PIG
21	98	7.6	897	1	CYRB_RABIT
22	96.5	7.5	378	1	ILIR_HUMAN
23	96	7.5	1165	1	LEPR_HUMAN
24	94	7.3	468	1	ILIR_MOUSE
25	92.5	7.2	638	1	GHR_RAT
26	92	7.2	2594	1	7LBS_DROVI
27	91	7.1	184	1	MPL_MPLV
28	91	7.1	608	1	PRUR_MOUSE
29	90	7.0	485	1	HXKA_YEAST
30	90	7.0	682	1	RECG_BACSU
31	89	6.9	638	1	GHR_MACMU
32	88.5	6.9	511	1	SCRB_ZYMKO
33	88	6.9	622	1	PRUR_HUMAN

## ALIGNMENTS

RESULT	ID	EPOR_HUMAN	STANDARD	PRT	508 AA.
AC	P19235	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Erythropoietin receptor precursor (EPO-R).				
GN	EPOR.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]	SEQUENCE FROM N.A.			
RP	MEDLINE=91372359; PubMed=1654273;				
RA	Ehrenman K., St John T.;				
RT	"The erythropoietin receptor gene: cloning and identification of				
RT	multiple transcripts in an erythroid cell line OCIW1.";				
RT	Exp. Hematol. 19:973-977(1991).				
RN	[2]	SEQUENCE FROM N.A.			
RP	MEDLINE=90304340; PubMed=2163696;				
RA	Jones S.S., D'Andrea A., Haines L.L., Wong G.G.;				
RT	"Human erythropoietin receptor: cloning, expression, and biologic				
RT	characterization.";				
RT	Blood 76:31-35(1990).				
RN	[3]	SEQUENCE FROM N.A.			
RP	TISSUE=Placenta;				
RC	MEDLINE=92399733; PubMed=1668606;				
RA	Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N.,				
RA	Hankins W.D.;				
RT	"Cloning of the human erythropoietin receptor gene.";				
RT	Blood 78:2548-2556(1991).				
RN	[4]	SEQUENCE OF 1-96 FROM N.A.			
RP	TISSUE=Placenta;				
RC	MEDLINE=92399734; PubMed=1668607;				
RA	Maouche L., Tournamille C., Hattab C., Boifa G., Carton J.P.,				
RA	Chretien S.;				
RT	"Cloning of the gene encoding the human erythropoietin receptor.";				
RT	Blood 78:2557-2563(1991).				
RN	[5]	SEQUENCE OF 1-17 FROM N.A.			
RP	MEDLINE=92147143; PubMed=1664413;				
RA	Penny L.A., Forget B.G.;				
RT	"Genomic organization of the human erythropoietin receptor gene.";				
RT	Genomics 11:974-980(1991).				
RN	[6]	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.			
RP	MEDLINE=96291992; PubMed=8662530;				
RA	Livshin O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S.,				
RA	Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.;				
RT	"Functional mimicry of a protein hormone by a peptide agonist: the				
RT	EPO receptor complex at 2.8 A.";				

34	88	6.9	845	1	CSW_DROME
35	87	6.8	610	1	PRUR_RAT
36	86.5	6.7	406	1	GSD_BACSU
37	85.5	6.7	805	1	SUST_SOYBN
38	85.5	6.7	863	1	AMPN_CAOCR
39	85.5	6.7	920	1	PARC_SYNY3
40	84.5	6.6	805	1	SUSY_PHAU
41	84.5	6.6	2561	1	PSL1_BACSU
42	84	6.5	336	1	CDIL_MOUSE
43	84	6.5	400	1	GMCR_HUMAN
44	84	6.5	485	1	HXKB_YEAST
45	84	6.5	1136	1	TIR1_BOVIN

P29349	drosophila
P05710	rattus norv
O32164	bacillus su
P13708	glycine max
P37807	caulobacter
P73077	synechocyst
O01390	phaeocyst
P33845	bacillus a
P11609	mus musculu
P15509	homo sapien
P04807	saccharomyc
O06805	bos taurus

```

RL Science273:464-471(1996).
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.
RX MEDLINB=99023198; PubMed=9608045;
RA Livnah O., Johnson D.L., Stura E.A., Farrell F.X., Barbone F.P.,
RA You Y., Liu K.D., Goldsmid M.A., He W., Krause C.D., Pestka S.,
RA Jolliffe L.K., Wilson I.A.;
RA Elliot S., Stoney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
RA Egrie J., Stroud R.M.;
RT "Efficiency of signalling through cytokine receptors depends
RT critically on receptor orientation";
RL Nature 395:511-516(1998).
CC -I- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC -----
DR EMBL, M34986; AAA52401.1; -.
DR EMBL, M60459; AAA52403.1; -.
DR EMBL, S45332; AAB23271.1; -.
DR EMBL, M76595; AAA52393.1; -.
DR EMBL, M77244; AAA52392.1; -.
DR PIR, A43799; A43799.
DR PIR, A49824; A49824.
DR PIR, A53958; A53958.
DR PDB, 1EBP; 29-JUL-97.
DR PDB, 1EBA; 18-NOV-98.
DR PDB, 1EER; 01-OCT-99.
DR PDB, 1CN4; 11-AUG-99.
DR MIM, 133171; -.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003528; Hematopo_receptor_I_FL.
DR Pfam, PF00041; fn3; 1.
DR SMART, SM00060; FN3; 1.
DR PROSITE, PS01352; HEMATOPO_REC_I_FL; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 508 ERYTHROPOIETIN RECEPTOR.
FT DOMAIN 25 250 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 251 273 POTENTIAL.
FT DOMAIN 274 508 CYTOPLASMIC (POTENTIAL).
FT DISULFID 148 213 FIBRONECTIN TYPE-III.
FT DISULFID 52 62
FT DISULFID 91 107
FT CARBOHYD 76 76 N-LINKED (GLCNAC, . .) (POTENTIAL).
SQ SEQUENCE 508 AA; 55065 MW; F9F326E12E9512A CRC64;

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D6	34	KFESKAALLAARCPBELLCTFERLEDLYCFEWEESAAGVGPNGNSFSFYQLEDEBPKLCRL	93
OY	61	HOAPPARGAATFMCOSLPADTSSFPVPELRLTAASGAPRHRHYTHINEVLLDAPVGLA	120
D6	94	HOAPRARGAVRFMCOSLPADTSSFPVPELRLVTAASGAPRHRHYTHINEVLLDAPVGLA	153
OY	121	RLADESGNVVTRMLPPEPTWTHSHRELDISAANGAGSVORVELLEGRTCYVLSNLRGR	180
D6	154	RLADESGNVVTRMLPPEPTWTHSHREVDVSAANGAGSVORVELLEGRTCYVLSNLRGR	213
OY	181	TRITIAVARARMAEPSCFGFMASMEEPVSLTT	211
D6	214	TRITIAVARARMAEPSCFGFMASMEEPVSLTT	244

RESULT	2			
EPOR_RAT				
ID	EPOR_RAT	STANDARD:	PRT:	507 AA.
AC	007303.			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last annotation update)			
DE	Erythropoietin receptor precursor (EPO-R).			
GN	EPOR.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Eumetazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93266574; PubMed=7684373;			
RA	Masuda S., Nagao M., Takahata K., Konishi Y., Gallyas F.,			
RA	Tahira T., Sasaki R.;			
RT	"Functional erythropoietin receptor of the cells with neural			
RT	characteristics. Comparison with receptor properties of erythroid			
RT	cells.";			
RL	J. Biol. Chem. 268:11208-11216(1993)			
CC	-1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE			
CC	MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION			
CC	AND DIFFERENTIATION.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.			
CC	-----			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; D13566; BAA02761.1; -.			
DR	PIR; A46713; A46713.			
DR	HSSP; P19235; IEBA.			
DR	InterPro; IPR002996; CRIA.			
DR	InterPro; IPR003961; FN.III.			
DR	InterPro; IPR003528; Hematopo_Receptor_L.F1.			
DR	Pfam; PF00041; In3; 1.			
DR	SMART; SM00060; FN3; 1.			
DR	PROSITE; PS01352; HEMATOPO_REC_L.F1; 1.			
KW	Receptor; Transmembrane; Glycoprotein; Signal.			
FT	SIGNAL	1	24	
FT	CHAIN	25	507	ERYTHROPOIETIN RECEPTOR.
FT	DOMAIN	25	249	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	250	272	POTENTIAL.
FT	DOMAIN	273	507	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	147	212	FIBRONECTIN TYPE-III.
FT	DISULFD	52	62	BY SIMILARITY.
FT	DISULFD	90	106	BY SIMILARITY.
FT	CARBOHD	75	75	N-LINKED (GLCNAC... ) (POTENTIAL).
SO	SEQUENCE	507 AA;	55499 MW;	ACT9A9E22D006A7312 CRC64;

Query Match	Similarity	68.3%:	Score 877.5:	DB 1:	Length 507:
Best Local	51.4%	Fred. No. 6.9e-69:			
Matches 165:	Conservative 23:	Mismatches 22:	Indels 1:	Gaps 1:	
QY	1	KFESEVALLAARGPELLCFTERTLEDIVOCFFEEASAGVPGNFSFSPOLJEDPMKRL	60		
DB	34	KFESEVALLAARGSELLCFTQRLLEDIVOCFFEEANSGMG-FNYSFSTQLEBESKRSCL	92		
QY	61	HOAPTRGALAIRFWCSLPTADTSSFPVLELRLLTAASGAPRHRVIRHINEVLLDAPVGLA	120		
DB	93	HOAPTRGSMRSMFWCSLPTADTSSFPVLELRQVTEAGSGSPYHRIHINEVLLDAPVGLA	152		
QY	121	RLADESGHVIVRWMPPETPMTHSHIRFELDLSAGAGAGVQVVELLEGTECVLSNLR	180		
DB	153	KRAEGSHVIVRWMPPAPMTTHIRYEDVDSAGNRAGOTOREVLEGRTECVLSNLRG	212		
QY	181	TRITAVRARMAPSPFGGFWMSAPSVLLT	211		
DB	213	TRYTFVAVRARMAPSPFGGFWMSAPSVLLT	243		
RESULT	3				
EPOR_MOUSE	STANDARD:	PRR:	507 AA.		
ID	EPOR_MOUSE	STANDARD:	PRR:	507 AA.	
AC	P14753: O63852;				
DT	01-APR-1990 (Rel. 14, Created)				
DT	01-APR-1990 (Rel. 14, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Erythropoietin receptor precursor (EPO-R).				
GN	EPOR.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid:10900;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=69195238; PubMed=2539263;				
RA	D'Andrea A.D., Lodish H.F., Wong G.G.;				
RT	"Expression cloning of the murine erythropoietin receptor.,"				
RL	Cell 57:277-285(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BALB/C; TISSUE=Liver;				
RX	MEDLINE=91080149; PubMed=2175360;				
RA	Kuramochi S., Ikawa Y., Todokoro K.;				
RT	"Characterization of murine erythropoietin receptor genes.,"				
RL	J. Mol. Biol. 216:567-575(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92017832; PubMed=1656233;				
RA	Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;				
RT	"Unregulated expression of the erythropoietin receptor gene caused by				
RT	insertion of spleen focus-forming virus long terminal repeat in a				
RL	murine erythroleukemia cell line.,"				
RN	Mol. Cell. Biol. 11:5527-5533(1991).				
RN	[4]				
RP	SEQUENCE OF 1-27 FROM N.A.				
RX	MEDLINE=90287158; PubMed=2162479;				
RA	Yousoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;				
RT	"Structure and transcription of the mouse erythropoietin receptor				
RT	gene.,"				
RL	Mol. Cell. Biol. 10:3675-3682(1990).				
RN	[5]				
RP	SEQUENCE OF 1-24 FROM N.A.				
RX	MEDLINE=91201346; PubMed=1849897;				
RA	Lacombe C., Christien S., Lemarchandel V., Mayeux P., Romeo P.H.;				
RA	Gisselbrecht S., Cartron J.P.;				
RT	"Spleen focus-forming virus long terminal repeat insertional				
RT	activation of the murine erythropoietin receptor gene in the T3C1-2				
RL	friend leukemia cell line.,"				
RN	J. Biol. Chem. 266:6952-6956(1991).				
RN	[6]				

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RESULT 4
TPOR_MOUSE STANDARD; PRT; 625 AA.
ID TPOR_MOUSE STANDARD; PRT; 625 AA.
AC 008351;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin receptor precursor (Tpo-R) (Myeloproliferative leukemia
DE protein) (C-mpl).
DE MPL OR TPOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93327753; PubMed=8334987;
RA Skoda R.C., Seidlin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,
RA Leder P.;
RT "Murine c-mpl: a member of the hematopoietic growth factor receptor
RT superfamily that transduces a proliferative signal.";
RL EMO J. 12:2645-2653(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ICF; TISSUE=Fetal liver;
RX MEDLINE=9330934; PubMed=8397366;
RA Vigon I., Florindo C., Fichelson S., Guenet J.-L., Mattei M.-G.,
RA Souvri M., Cosman D., Gisselbrecht S.;
RT "Characterization of the murine Mpl proto-oncogene, a member of the
RT hematopoietic cytokine receptor family: molecular cloning,
RT chromosomal location and evidence for a function in cell growth.";
RL Oncogene 8:2607-2615(1993).
CC -1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: Z22649; CA80365.1; -
DR EMBL: Z22657; CA80372.1; -
DR EMBL: X73677; CA52031.1; -
DR PIR: S3517; S3517.
DR HSSP: P19235; 1EBA.
DR MGD: MGI:97076; Mpl.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_FL.
DR SMART: SM0060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_FL; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNL 1 25 POTENTIAL.
FT CHAIN 26 625 THROMBOPOIETIN RECEPTOR.
FT DOMAIN 26 482 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 483 504 POTENTIAL.
FT DOMAIN 505 625 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 99 8 MISSING (IN REF. 2).
FT CONFLICT 99 99 D->V (IN REF. 2).
FT CONFLICT 222 222 P->V (IN REF. 2).
FT CONFLICT 222 222 P->V (IN REF. 2).
SQ SEQUENCE 625 AA; 69817 MW; 309CF6EAA3724549 CRC64;

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Query Match 13.3%; Score 171; DB 1; Length 625;  
Best Local Similarity 24.6%; Pred. No. 2,4e-07;

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Matches 62; Conservative 33; Mismatches 105; Indels 52; Gaps 8;
QY 4 SKAALLAARGPERILGTERIEDLVCFEEASAGVPGNFSPQLEDEPMKLCRIHQ 63
QY 25 SQVFLALGTEPLNEFSQFFEDLTCFMBDEEAA--PSGIYQLLVYRGKPRACPLYSQ 82
QY 64 P7ARGAIFWCSLPTAD-TSSEVPLELRITLAA-GAPRRHVRHINEVILLDAPVLYAR 121
QY 83 SVPTFGRRVYVCPADDEVLFPLHLWKNVSLNLTLLORVLFVDSVGLPAPRVYIKAR 142
QY 122 LADESGHYVIRW-LPPETPMTHIRELDI-----SAGNGAGSVQVVELLEGRT----- 170
QY 143 GGSQPGELQLHWEAPAE--ISDFLRHELKYGPTDSSNATAPSV--TQLSTCCPTLM 198
QY 171 -----ECVLSNLGRTRITRTIIVARMAEPPSG 197
QY 199 MRPNPVYLQPCVHPHTASQPHGPAPFLVYKGGSCSLVSLQAKSYWLQLRSPDGVSLR 258
QY 198 GFWSANSEPVSL 209
QY 259 GSWGPMSEFPVTV 270
Db 198 GFWSANSEPVSL 209
Db 259 GSWGPMSEFPVTV 270
RESULT 5
TPOR_HUMAN STANDARD; PRT; 635 AA.
ID TPOR_HUMAN STANDARD; PRT; 635 AA.
AC P40238;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin receptor precursor (Tpo-R) (Myeloproliferative leukemia
DE protein) (C-mpl) (Cd110 antigen).
DE MPL OR TPOR.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92302297; PubMed=1608974;
RA Vigon I., Morron J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
RA Gisselbrecht S., Souvri M.;
RT "Molecular cloning and characterization of MPL, the human homolog of
RT the v-mpl oncogene: identification of a member of the hematopoietic
RT growth factor receptor superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292186; PubMed=8020956;
RA Mignotte V., Vigon I., de Crevecoeur E., Romeo P.H., Lemarchandel V.,
RA Chretien S.;
RT "Structure and transcription of the human c-mpl gene (MPL).";
RL Genomics 20:5-12(1994).
CC -1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: C-MPL-K (SHOWN HERE) AND C-MPL-
CC P; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT A LOW LEVEL IN A LARGE NUMBER OF
CC CELLS OF HEMATOPOIETIC ORIGIN. THE TWO FORMS (C-MPL-K AND C-MPL-
CC P) ARE ALWAYS FOUND TO BE COEXPRESSED.
CC -1- DISEASE: DEFECTS IN MPL ARE A CAUSE OF CONGENITAL AMEGAKARYOCYTIC
CC THROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED BY ISOLATED
CC THROMBOCYTOPENIA AND MEGAKARYOCYTOPENIA WITH NO PHYSICAL
CC ANOMALIES.
CC -1- SIMILARITY: BELONGS TO THE CYOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-8 IS THE INITIATOR.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD10 entry;
CC WWW=http://www.ncbi.nlm.nih.gov/prov/guide/11586825.g.htm.
CC -----
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RESULT	6	
PRLR_BOVIN		
ID	PRLR_BOVIN	STANDARD;
AC	Q28172;	PRT; 581 AA

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Polactin receptor precursor (PRL-R).  
 GN PRLR.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;  
RN  
RP  
RC  
RT TISSUE=Endometrium;  
RX MEDLINE=93246019; PubMed=1338725;  
RA Scott P., Kessler M.A., Schuler L.A.;  
RT "Molecular cloning of the bovine prolactin receptor and distribution  
of prolactin and growth hormone receptor transcripts in fetal and  
uterine-placental tissues.";  
LT Mol. Cell. Endocrinol. 89:47-58(1992).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
CC PROLACTIN.  
CC  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC  
CC  
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CC  
CC EMBL, J02549; AAA51A17.1; -.  
DR HSSP: P14787; IAN.  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003528; Hematopo\_receptor\_Lc\_F1.  
CC

DR	Plam; PF00041; In5; 4.
DR	SMART; SM00060; FN3; 2.
DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW	Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT	SIGNAL 1 24
FT	CHAIN 25 581
FT	DOMAIN 25 234
FT	TRANSMEM 235 258
FT	DOMAIN 259 581
FT	DOMAIN 25 122
FT	PROLACTIN RECEPTOR. POTENTIAL.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).
FT	FIBROBLAST TYPE-III 1.

Query Match	Score	DB 1	Length	DB 2
FT DOMAIN	123	227	FIBRONECTIN TYPE-III 2.	
FT DISUFID	36	46	BY SIMILARITY.	
FT CARBOHYD	75	86	N-LINKED (GICNAC . . . ) (POTENTIAL).	
FT CARBOHYD	59	59	N-LINKED (GICNAC . . . ) (POTENTIAL).	
FT CARBOHYD	132	132	N-LINKED (GICNAC . . . ) (POTENTIAL).	
SEQUENCE	581 AA.	65153 MW.	7385C0D6556E139 CMC64.	

[illegible]



CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND SECRETED.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: M84747; AAA58679.1; -  
DR EMBL: S71404; AAB30844.2; ALT\_SEQ.  
DR EMBL: S71420; AAD14081.1; -  
DR EMBL: L39064; AAC29513.1; -  
DR PIR: B45268; B45268.  
DR MIM: 300007; -  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003531; Hematopo\_receptor\_S\_F1.  
DR PROSITE: PS01355; HEMATOPO\_REC\_S\_F1; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 40  
FT CHAIN 41 522 INTERLEUKIN-9 RECEPTOR.  
FT DOMAIN 41 270 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 271 291 POTENTIAL.  
FT DOMAIN 292 522 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 150 244 FIBRONECTIN TYPE-III.  
FT DOMAIN 429 439 POLY-ASN.  
FT DOMAIN 440 443 POLY-ASN.  
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 331 331 R -> G (IN REF. 3).  
FT CONFLICT 439 439 MISSING (IN REF. 3).  
SQ SEQUENCE 522 AA; 57333 MW; ECBC5C6342DE2BB2 CRC64;  
  
Query Match 8.9%; Score 114.5; DB 1; Length 522;  
Best Local Similarity 22.1%; Pred. No. 0.016;  
Matches 61; Conservative 32; Mismatches 110; Indels 73; Gaps 12;  
  
QY 12 KGPPEE-ILCTFERLDVCFEEAASAGVGPNGSFSQLDEDEPKLCRLQAAPTARGA 69  
DB 47 QGPRSRFTCTLNITIRICHN-SAPELQOG-----SSPWLFTSQAPGCTHK 94  
QY 70 IFWCSLPRTADSSFPVLELRITLTAASG-APRFRHVHINEV-----VLDDAP 115  
DB 95 ----CILRSECTVAVLPPEAVLVPSNDFTITFHCHMSGRQVSLVDPEYLPRRHVKLDDP 150  
QY 116 VGLVARLADESGHVAVIRW-LPPPEPMTSHIRFELDLSAGNGA-GSVQREVLLEGRTCEV 173  
DB 151 SPLQSNIS--SGHCILTWISIPALREMTLLSYELAFKQOEAWEDQAQRDHVGYTWLI 208  
QY 174 LSNL-----RGRTITIAVRAR--MAEPSFGGFWASMESEPV----- 208  
DB 209 LEAFELDPGFIHEARLRVMTLEDDVVEERYTGQMSQVPCVQAPQROGRLIPWG 268  
QY 209 -----LITGGGSSRMKELEOKYKELLRN 232  
DB 269 WPGNTLVAVSIFLLLTGPLYFLKLSPRVKRIEYON 304  
  
RESULT 9  
GHR\_BOVIN  
ID GHR\_BOVIN STANDARD; PRT; 634 AA.  
AC P79108;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE Growth hormone receptor precursor (GH receptor) (Serum binding  
DE protein).  
GN GHR.  
OS Bos taurus (Bovine).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
CC Bovidae; Bovinae; Bos.  
CC NCBI\_TaxId=9913;  
CC [1]  
CC SEQUENCE FROM N.A.  
CC STRAIN=GITR; TISSUE=liver;  
CC Souza S.C., Wang X., Lobo R.B., Kopichek J.J.;  
CC Submitted (Jul-1994) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
CC -----  
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CC -----  
DR EMBL: X70041; CAA49635.1; -  
DR HSSP: P10912; 1HMH.  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003528; Hematopo\_receptor\_L\_F1.  
DR Pfam: PF00041; fn3; 1.  
DR SMART: SM00060; FN3; 1.  
DR PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 634 GROWTH HORMONE RECEPTOR.  
FT DOMAIN 19 260 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 261 284 POTENTIAL.  
FT DOMAIN 285 634 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 141 248 FIBRONECTIN TYPE-III.  
FT DISULFID 56 66 BY SIMILARITY.  
FT DISULFID 97 108 BY SIMILARITY.  
FT DISULFID 122 136 BY SIMILARITY.  
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 634 AA; 70979 MW; 91955A28296CBD2E CRC64;  
  
Query Match 8.8%; Score 112.5; DB 1; Length 634;  
Best Local Similarity 26.3%; Pred. No. 0.029;  
Matches 35; Conservative 25; Mismatches 60; Indels 13; Gaps 5;  
  
QY 14 PEELICTFERLDVCFEEAASAGV-GPGNS-FSQLDEDEPKLCRLQAAPTARGAIR 71  
DB 51 PKFTKCRSPLELTFSCWMTDGANHSQSGVQMFYIRIDIDEMKEC-----PDVYSAGE 105  
QY 72 FWCSLPRTADSSFPVLELRITLTAASGAPRFRHVHINEVVLDDAPGLVARLADES----- 126  
DB 106 NSCYFNSSTYSVWTPCYIKLITNSGIVD-HKCFSEVDIVQDPDPVGLMNTLNLISLSTEIH 164  
QY 127 GHVAVIRMLPPPEP 139  
DB 165 ADILVAKWPPPPNT 177  
  
RESULT 10  
GHR\_SHEEP  
ID GHR\_SHEEP STANDARD; PRT; 634 AA.  
AC Q28575;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Growth hormone receptor precursor (GH receptor) (Serum binding  
DE protein).  
GN GHR.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=91099608; PubMed=1980117;  
RA Adams T.E., Baker L., Fiddes R.J., Brandon M.R.;  
RT "The sheep growth hormone receptor: molecular cloning and ontogeny of  
RT mRNA expression in the liver."  
RT Mol. Cell. Endocrinol. 73:135-145(1990).  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
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CC -----  
DR EMBL: M82912; AAA73171.1; -.  
DR HSSP: P10912; IAX1.  
DR InterPro: IPR002996; CRA.  
DR InterPro: IPR003961; FN.III.  
DR InterPro: IPR003528; Hematopo\_receptor\_L\_F1.  
DR Pfam: PF00041; fn3; 1.  
DR SMART: SM00060; FN3; 1.  
DR PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; 1.  
DR Receptor: Transmembrane; Glycoprotein; Signal.  
KW SIGNAL 1 18  
FT CHAIN 19 634 GROWTH HORMONE RECEPTOR.  
FT DOMAIN 19 260 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 261 284 POTENTIAL.  
FT DOMAIN 285 634 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 141 248 FIBRONECTIN TYPE-III.  
FT DISULFID 56 66 BY SIMILARITY.  
FT DISULFID 97 108 BY SIMILARITY.  
FT DISULFID 122 136 BY SIMILARITY.  
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 634 AA; 70844 MW; FFD28B9C23EC1496 CRC64;  
  
Query Match 8.6%; Score 110.5; DB 1; Length 634;  
Best Local Similarity 26.6%; Pred. No. 0.044; Mismatches 57; Indels 13; Gaps 5;  
Matches 34; Conservative 24;  
  
OY 19 CFTERLEDLVCFFEEASAGV-GPGNFS-PSFOLEDEPMKLCRLHOAPTARGAIREWCSTL 76  
DB 56 CRSPLELETFSCHWMTGDANSHLSQSGVQMYIRRDIOEWKEC-----PDVVSAGENCYF 110  
OY 77 PTADTSSFVPLELRVLAASAPRFRHYVINEVLLDAPVGLVARLADES-----GHVVI 131  
DB 111 NSSYTSVWTFYCIKITSNGIIVD-HKCFSEVDIVQDPVGLMNTLINTLITETIHADILV 169  
OY 132 RMLPPPET 139  
DB 170 KWPPPPPT 177

RESULT 11  
ID PRLR.CHICK  
AC 004594; STANDARD; PRT; 831 AA.  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Prolactin receptor precursor (PRL-R) (CPRLP).  
GN PRLR.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WHITE LEGHORN; TISSUE=Kidney;  
RX MEDLINE=93075121; PubMed=1445292;  
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;  
RT "Double antenna structure of chicken prolactin receptor deduced from  
RT the cDNA sequence."  
RT Biochem. Biophys. Res. Commun. 188:490-496(1992).  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
CC PROLACTIN.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.  
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CC -----  
DR EMBL: D13154; BAA02439.1; -.  
DR PIR: J01655; J01655.  
DR HSSP: P14787; IAN3.  
DR InterPro: IPR002996; CRA.  
DR InterPro: IPR003961; FN.III.  
DR InterPro: IPR003528; Hematopo\_receptor\_L\_F1.  
DR Pfam: PF00041; fn3; 4.  
DR SMART: SM00060; FN3; 3.  
DR PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; 1.  
DR Receptor: Transmembrane; Glycoprotein; Signal; Repeat.  
KW SIGNAL 1 23  
FT CHAIN 24 831  
FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 439 459 POTENTIAL.  
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.  
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.  
FT DISULFID 36 46 BY SIMILARITY.  
FT DISULFID 75 86 BY SIMILARITY.  
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 831 AA; 94102 MW; 1CAE7591DCADBE9 CRC64;  
  
Query Match 8.6%; Score 110; DB 1; Length 831;  
Best Local Similarity 21.5%; Pred. No. 0.067;







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FT DOMAIN 17 237 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 238 261 POTENTIAL.
FT DOMAIN 252 608 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 117 223 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 72 83 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 608 AA; 68572 MW; D7IAD/B6C62528DC CRC64;

Query Match 8.3%; Score 107; DB 1; Length 608;
Best Local Similarity 26.7%; Pred. No. 0.084; Indels 33; Gaps 9;
Matches 54; Conservative 26; Mismatches 90;

OY 14 PELLCTERLEDVCFEEAASAGVPGNFSFSQL-----EDEPKLCRLHOAPFANG 68
DB 29 PQISKCRSPLETFSCYWD-----GKVTSGTIQLMKRSDDEMKEC-----PDYIT 77

OY 69 AIRFCSLPADTSSFPVLELRLTAASGAPRRHVIHNEVLLDAPVGLVARLADES-- 126
DB 78 AGENSCYFNTSYTSIMIPYCVKL-ANKDEVPEDEKCFSDVEIYLPDPVHLNMTLNTSQT 136

OY 127 ---GHVIRWLPDPPTDMS---HIRELDISAGNGAGSVQVELLEGTECV--LSNR 178
DB 137 GIHGDIQVWMDPPPTADYQKMTTLEYELQYKEVNET---KWELEPLRLSTVPLYSIK 192

OY 179 GRTRTIYAVRARM-AEPSFGF 199
DB 193 MGRDYEIRVRSRQRTSEKGEF 214

RESULT 15
GHR.COLLI STANDARD; PRT; 611 AA.
AC Q90375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
  protein).
GN GHR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columidae; Columba.
OX NCBI_TaxID=9932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.F.;
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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-----
CC EMBL: U20353; AAA84745.1; -.
DR HSSP: P10912; IAXI.
DR InterPro: IPR002896; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.

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DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 611 GROWTH HORMONE RECEPTOR.
FT DOMAIN 21 240 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 241 264 POTENTIAL.
FT DOMAIN 265 611 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 119 226 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT DISULFID 100 114 BY SIMILARITY.
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 611 AA; 68851 MW; C48750BF9EE4BDA CRC64;

Query Match 8.1%; Score 104.5; DB 1; Length 611;
Best Local Similarity 26.2%; Pred. No. 0.14;
Matches 53; Conservative 28; Mismatches 96; Indels 25; Gaps 10;

OY 12 RGPPELLCTERLEDVCFEEAASAGV-GPGNFSF-QLEDPEPKLCRLHOAPFANG 69
DB 27 RLPQISKCRSPLETFSCYWDGNGFNYSAPGTIQLMKRDEDEMKEC-----PDYITA 81

OY 70 IRFWCSLPADTSSFPVLELRLTAASGAPRRHVIHNEVLLDAPVGLVARLADES-- 126
DB 82 GENSCYFNTSYTSIMIPYCVKLVNDEV--PDEKCSVDVEIYLPDPVHLNMTLNTSQT 139

OY 127 ---GHVIRWLPDPPTDMS---HIRELDISAGNGAGSVQVELLEGTECV--LSNR 178
DB 140 GIHGDIQVWMDPPPTADYQKMTTLEYELQYKEVNET---KWELEPLRLSTVPLYSIK 195

OY 179 GRTRTIYAVRARM-AEPSFGF 199
DB 196 IGRDYEIRVRSRQRTSEKGEF 217

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Search completed: August 28, 2002, 17:40:43  
 Job time: 534 sec

